```
  1  GAATTCCAGGCTGCTAGGAAGTGAAAAGTGAACCTGGACCCAGCTCAGCGGCAGCAGCAG   60

 61  CGGCAGCAGGCAGCAGCCTCTATCCTCTCCTCCAGCCACATGGCCCCCGGATGGCGCTT   120
                                         MetGlyProArgMetAlaLeu

121  CCCCGCGTGCTCCTGCTCCTGTTCTTGCACCTGTTGCTGCTAGGATGCCGTTCCCATCCA  180
     ProArgValLeuLeuLeuLeuPheLeuHisLeuLeuLeuLeuGlyCysArgSerHisPro
     eProAlaCysSerCysSerCysSerCysThrCysCysCysEndAspAlaValProIleHi
     erProArgAlaProAlaProValLeuAlaProValAlaAlaArgMetProPheProSerT

181  CTGGGTGGCGCTGGCCTGGCCTCAGAACTGCCAGGGATACAGGTGAGCCCTGATGAACTG  240
     LeuGlyGlyAlaGlyLeuAlaSerGluLeuProGlyIleGlnValSerProAspGluLeu
     sTrpValAlaLeuAlaTrpProGlnAsnCysGlnGlyTyrArgEndAlaLeuMetAsnCy
     hrGlyTrpArgTrpProGlyLeuArgThrAlaArgAspThrGlyGluProEndEndThrA

241  CTTAGACTTGGTTGGCTGGGAGGGCGCGGACAGCAGCAACTAACGGGTCCCCACCTACTG  300
     LeuArgLeuGlyTrpLeuGlyGlyArgGlyGlnGlnGlnLeuThrGlyProHisLeuLeu
     sLeuAspLeuValGlyTrpGluGlyAlaAspSerSerAsnEndArgValProThrTyrCy
     laEndThrTrpLeuAlaGlyArgAlaArgThrAlaAlaThrAsnGlySerProProThrV
```

FIG. 1A

```
301  TTCCAAGAGGGCTCTAACCTCCTTTGGGAACTAGTGATAAGGGGTTTAGAAGGCAGCCAG  360
     PheGlnGluGlySerAsnLeuLeuTrpGluLeuValIleArgGlyLeuGluGlySerGln
     sSerLysArgAlaLeuThrSerPheGlyAsnEndEndEndGlyValEndLysAlaAlaAr
     alProArgGlyLeuEndProProLeuGlyThrSerAspLysGlyPheArgArgGlnProG

361  GCTGGGGGTGAGGACCCGCTCCCAAGGCAGTTGGTTCGCTTCAGCACCATCAAGAGTGAT  420
     AlaGlyGlyGluAspProLeuProArgGlnLeuValArgPheSerThrIleLysSerAsp
     gLeuGlyValArgThrArgSerGlnGlySerTrpPheAlaSerAlaProSerArgValMe
     lyTrpGlyEndGlyProAlaProLysAlaValGlySerLeuGlnHisHisGlnGluEndT

421  GGGTCCAGGTGCGAGTTCCTGAGGCTCGGGCTCCCCCACCCATCCCAGGAGCTGCTGGAC  480
     GlySerArgCysGluPheLeuArgLeuGlyLeuProHisProSerGlnGluLeuLeuAsp
     tGlyProGlyAlaSerSerEndGlySerGlySerProThrHisProArgSerCysTrpTh
     rpValGlnValArgValProGluAlaArgAlaProProProIleProGlyAlaAlaGlyP

481  CGCCTGCGAGACAGGGTCTCCGAGCTGCAGGCGACGGGACGGACCTGGAGCCCCTCCGGC  540
     ArgLeuArgAspArgValSerGluLeuGlnAlaThrGlyArgThrTrpSerProSerGly
     rAlaCysGluThrGlySerProSerCysArgArgArgAspGlyProGlyAlaProProAl
     roProAlaArgGlnGlyLeuArgAlaAlaGlyAspGlyThrAspLeuGluProLeuArgG

541  AGGACCGTGGCCTCACAGAAGCCTGGGAGGCGAGGGAAGCAGCCCCCACGGGGGTTCTTG  600
     ArgThrValAlaSerGlnLysProGlyArgArgGlyLysGlnProProArgGlyPheLeu
     aGlyProTrpProHisArgSerLeuGlyGlyGluGlySerSerProHisGlyGlySerTr
     lnAspArgGlyLeuThrGluAlaTrpGluAlaArgGluAlaAlaProThrGlyValLeuG
```

FIG. 1B

```
601  GGCCCCGCAGTAGCATCTTCCAAGTCCTCCGGGAATACGCAGCCCCAAGACGATGCGTG  660
     GlyProAlaValAlaSerSerLysSerSer
     pAlaProGlnEndHisLeuProSerProPro
     lyProArgSerSerIlePheGlnValLeuArgGlyIleArgSerProLysThrMetArgA

661  ACTCTGGCTGCTTTGGCGGAGGCTGGACCGGATCGGCTCCCTCAGCGGCCTGGGCTGCA  720
     spSerGlyCysPheGlyArgArgLeuAspArgIleGlySerLeuSerGlyLeuGlyCysA

721  ATGGTGAGCACCCACCCCATTCCCACTGCACGCCCCGGTTAGCATCACTTCTGGGTTTGA  780
     snV

781  TGTCTCTGGGACCAAACTCCGAGAAAAGGACACCTGGATATCACTCTTTCTTGTTGCCAG  840

841  TCCTCAAGGCCAAGGAGCGCCTTCCTGGAAAAATTAAATTTGGACAGCATTCACTAGCAT  900

901  GACTATGAGTCCCCACCCACCTTCTCGCCACCCCCTGCCTCTCTCACCCAAGGCGGCAGA  960

961  ATTACTTTAGGATGTAAATTCTGTCATTGCCTGGCTGCCGCTCCTGGAGCAAAAAGAGA  1020
```

FIG. 1C

1021 ACTAAACCTCTTCCCCCTGGTTTCCCCTCAACTGTCTGTGGCTGCAAAGGCAGAGGGCAG 1080

1081 GATCACCAGGGTGATGACAAGTCCCAGCTTACAAGGAGGAAACTCAGGTCCAGAGAGATG 1140

1141 GATTATCCCAAAGCCCCAAACATCCAGTTCTGCTGAAGAAGGCGGGTGGCAGGGGTGGCA 1200

1201 CGTGGTGGGGGGAAGCCCAGGTCCTGCCTGCCTCTCACCCTAATGTCATCCTCACCCTCT 1260

1261 CTCTCCCCCCCACAGTGCTCAGGAGGTACTGAGAAGTCCTGGCTGACAACCTCTGTGTCC 1320

alLeuArgArgTyr***

1321 GCTTCTCCAACGCCCCTCCCCTGCTCCCCTTCAAAGCAACTCCTGTTTTTATTTATGTAT 1380

1381 TTATTTATTTATTTATTTGGTGGTTGTATATAAGACGGTTCTTATTTGTGAGCACATTTT 1440

1441 TTCCATGGTGAAATAAAGTCAACATTAGAGCTCTGTCTTTTGAAAAAAAAAAAAAAAGGA 1500

1501 ATTC 1504

FIG.1D

BNP Screening Oligos

```
5'-TCCAGCTGCTTCGGGGGCAGGATGGACAGGATTGGAGCCCAGAGCGGACTGGGCTGTAAC-3'   human ANP
   SerSerCysPheGlyGlyArgMetAspArgIleGlyAlaGlnSerGlyLeuGlyCysAsn-3'   human ANP
   (2)                                                  (21)
   SerGlyCysPheGlyArgArgLeuAspArgIleGlySerLeuSerGlyLeuGlyCysAsn      pig BNP
5'-ACNGGNTGCTTGGGNCGNCGNCTNGACCGNATNGGNTCNCTNTCNGGNCTNGGNTGCAAC-3'   Pig BNP
   TG     T  A   A  A  T    TA       AG T  AG    T      T  T

3'-AGGCCGACGAAGCCCGCGTCCGACCTGTCCTAACCTAGGGACTCGCCTGACCCGACATTG-5' 3351  (minimal)

3'-TCGCCGACGAAGCCGTCTTCTGAGCTGTCTTAGCCGTCGGAGTCGCCGGAGCCGACGTTG-5' 3352  (G/T pref)

3'-AGGTCGACGAAGCCCCCGTCCTACCTGTCCTAACCTCGGGTCTCGCCTGACCCGACATTG-5' 3376  (ANP)
```

FIG.2

hn BNP cDNA (10-13-88)

```
  1  GAATTCCAGGCTGCTAGGAAGTGAAAAGTGAACCTGGACCCAGCTCAGCGGCAGCAGCAGCGGCAGCAGG   70

 71  CAGCAGCCTCTATCCTCTCCTCCAGCCACATGGGCCCCCGGATGGCGCTTCCCCGCGTGCTCCTGCTCCT  140
                                    MetGlyProArgMetAlaLeuProArgValLeuLeuLeuLe

141  GTTCTTGCACCTGTTGCTGCTAGGATGCCGTTCCCATCCACTGGGTGGCGCTGGCCTGGCCTCAGAACTG  210
     uPheLeuHisLeuLeuLeuLeuGlyCysArgSerHisProLeuGlyGlyAlaGlyLeuAlaSerGluLeu
                                         -1 +1                          10

211  CCAGGGATACAGGTGAGCCCTGATGAACTGCTTAGACTTGGTTGGCTGGGAGGGCGCGGACAGCAGCAAC  280
     ProGlyIleGln

281  TAACGGGTCCCCACCTACTGTTCCAAGAGGGCTCTAACCTCCTTTGGGAACTAGTGATAAGGGGTTAGAA  350

351  GGCAGCCAGGCTGGGGGTGAGGACCCCGCTCCCAAGGCAGTTGGTTCGCTTCAGCACCATCAAGAGTGAT  420

421  GGGTCCAGGTGCGAGTTCCTGAGGCTCGGGCTCCCCCACCCATCCCAGGAGCTGCTGGACCGCCTGCGAG  490
                                                        GluLeuLeuAspArgLeuArgA
                                                                    20.

491  ACAGGGTCTCCGAGCTGCAGGCGGAGCGGACGGACCTGGAGCCCCTCCGGCAGGACCGTGGCCTCACAGA  560
     spArgValSerGluLeuGlnAlaGluArgThrAspLeuGluProLeuArgGlnAspArgGlyLeuThrGl
                   30.                            40.

561  AGCCTGGGAGGCGAGGGAAGCAGCCCCCACGGGGGTTCTTGGGCCCCGCAGTAGCATCTTCCAAGTCCTC  630
     uAlaTrpGluAlaArgGluAlaAlaProThrGlyValLeuGlyProArgSerSerIlePheGlnValLeu
```

FIG.3A

```
              50.        .        .       60.        .         70.
631   CGGGGAATACGCAGCCCCAAGACGATGCGTGACTCTGGCTGCTTTGGGCGGAGGCTGGACCGGATCGGCT   700
      ArgGlyIleArgSerProLysThrMetArgAspSerGlyCysPheGlyArgArgLeuAspArgIleGlyS
              .   ↑1           80.↑2     .        .       90.        .
701   CCCTCAGCGGCCTGGGCTGCAATGGTGAGCACCCACCCCCATTCCCACTGCACGCCCCGGTTAGCATCAC   770
      erLeuSerGlyLeuGlyCysAsnV
              .  100        .        .        .        .        .
771   TTCTGGGTTTGATGTCTCTGGGGACCAAACTCCGAGAAAAGGACACCTGGATATCACTCTTTCTTGTTGC   840
              .        .        .        .        .        .        .
841   CAGTCCTCAAGGCCAAGGAGCGCCTTCCTGGAAAAATTAAATTTGGACAGCATTCACTAGCATGACTATG   910
              .        .        .        .        .        .        .
911   AGTCCCCACCCACCTTCTCGCCACCCCCTGCCTCTCTCACCCAAGGCGGCAGAATTACTTTAGGATGTAA   980
              .        .        .        .        .        .        .
981   ATTCTGTCATTGCCTGGCTGCCGCTCCTGGGAGCAAAAAGAGAACTAAACCTCTTCCCCCTGGTTTCCCC   1050
              .        .        .        .        .        .        .
1051  TCAACTGTCTGTGGCTGCAAAGGCAGAGGGCAGGATCACCAGGGTGATGACAAGTCCCAGCTTACAAGGA   1120
              .        .        .        .        .        .        .
1121  GGAAACTCAGGTCCAGAGAGATGGATTATCCCAAAGCCCCAAACATCCAGTTCTGCTGAAGAAGGCGGGT   1190
              .        .        .        .        .        .        .
1191  GGCAGGGGTGGCACGTGGTGGGGGAAGCCCAGGTCCTGCCTGCCTCTCACCCTAATGTCATCCTCACCC   1260
              .        .        .        .        .        .        .
1261  TCTCTCTCCCCCCCACAGTGCTCAGGAGGTACTGAGAAGTCCTGGCTGACAACCTCTGTGTCCGCTTCTC   1330
                       alLeuArgArgTyr***
              .        .      106        .        .        .        .
1331  CAACGCCCCTCCCCTGCTCCCCTTCAAAGCAACTCCTGTTTTTATTTATGTATTTATTTATTTATTTATT   1400
              .        .        .        .        .        .        .
1401  TGGTGGTTGTATATAAGACGGTTCTTATTTGTGAGCACATTTTTTCCATGGTGAAATAAAGTCAACATTA   1470
              .        .        .
1471  GAGCTCTGTCTTTTGAAAAAAAAAAAAAAAGGAATTC   1507
```

FIG.3B

Mature Pig BNP cDNA (10-13-88)

```
1    GAATTCCAGGCTGCTAGGAAGTGAAAAGTGAACCTGGACCCAGCTCAGCGGCAGCAGCAGCGGCAGCAGG   70

71   CAGCAGCCTCTATCCTCTCCTCCAGCCACATGGGCCCCCGGATGGCGCTTCCCCGCGTGCTCCTGCTCCT   140
                                  MetGlyProArgMetAlaLeuProArgValLeuLeuLeuLe

141  GTTCTTGCACCTGTTGCTGCTAGGATGCCGTTCCCATCCACTGGGTGGCGCTGGCCTGGCCTCAGAACTG   210
     uPheLeuHisLeuLeuLeuLeuGlyCysArgSerHisProLeuGlyGlyAlaGlyLeuAlaSerGluLeu
          ↓1
211  CCAGGGATACAGGAGCTGCTGGACCGCCTGCGAGACAGGGTCTCCGAGCTGCAGGCGGAGCGGACGGACC   280
     ProGlyIleGlnGluLeuLeuAspArgLeuArgAspArgValSerGluLeuGlnAlaGluArgThrAspL

281  TGGAGCCCCTCCGGCAGGACCGTGGCCTCACAGAAGCCTGGGAGGCGAGGGAAGCAGCCCCCACGGGGGT   350
     euGluProLeuArgGlnAspArgGlyLeuThrGluAlaTrpGluAlaArgGluAlaAlaProThrGlyVa

351  TCTTGGGCCCCGCAGTAGCATCTTCCAAGTCCTCCGGGGAATACGCAGCCCCAAGACGATGCGTGACTCT   420
     lLeuGlyProArgSerSerIlePheGlnValLeuArgGlyIleArgSerProLysThrMetArgAspSer
                                                                    ↓2
421  GGCTGCTTTGGGCGGAGGCTGGACCGGATCGGCTCCCTCAGCGGCCTGGGCTGCAATGTGCTCAGGAGGT   490
     GlyCysPheGlyArgArgLeuAspArgIleGlySerLeuSerGlyLeuGlyCysAsnValLeuArgArgT

491  ACTGAGAAGTCCTGGCTGACAACCTCTGTGTCCGCTTCTCCAACGCCCCTCCCCTGCTCCCCTTCAAAGC   560
     yr***

561  AACTCCTGTTTTTATTTATGTATTTATTTATTTATTTATTTGGTGGTTGTATATAAGACGGTTCTTATTT   630

631  GTGAGCACATTTTTTCCATGGTGAAATAAAGTCAACATTAGAGCTCTGTCTTTTGAAAAAAAAAAAAAAA   700

701  GGAATTC   707
```

FIG.4

Dog BNP Gene 12-12-88

```
  1 CGATCAGGGATGTTGGGGCGGAGGAAACGGAGGGAAGGAGGGAGCGGAGGAGGCCCGAGGACTGTTGGTG  70

 71 TCCCCCTCCTGCCCTTTTGGGGCCAGGCCCACTTCTATACAAGGCCTGCTCTCCAGCCTCCACCCCGGCG 140

141 GGTATGGTGCAGGCGCGGAGGGGCGCATTCCCCCGCCCTGAGCTCAGCGGCCGGAATGCGGCCGATAAAT 210

211 CAGAGATAACCCCAGGCGCGGGATAAGGGATAAAAAGCCCCCGTTGCCGCGGGATCCAGGAGAGCACCCG 280

281 CGCCCCAAGCGGTGACACTCGACCCCGGTCGCAGCGCAGCAGCTCAGCAGCCGGACGTCTCTTTCCCCAC 350

351 TTCTCTCCAGCGACATGGAGCCCTGCGCAGCGCTGCCCCGGGCCCTCCTGCTCCTCCTGTTCTTGCACCT 420
                  MetGluProCysAlaAlaLeuProArgAlaLeuLeuLeuLeuLeuPheLeuHisLe

421 GTCGCCACTCGGAGGCCGCCCCCACCCGCTGGGCGGCCGCAGCCCCGCCTCGGAAGCCTCGGAAGCCTCA 490
    uSerProLeuGlyGlyArgProHisProLeuGlyGlyArgSerProAlaSerGluAlaSerGluAlaSer

491 GAAGCCTCGGGGTTGTGGGCCGTGCAGGTGAGCGCTCAGCCTGCCTGAAGGCCGCGGCGGGTGGCAGCAG 560

561 GTCACGGGGGCTTAGCCACTGTCCCAAGTCCTCAGTCTCCCTTGGGAATTAGTGATAAGGGAATCAGAAA 630

631 GTGACGAGATTGGGTGCCAGGACTCCATACCCAAGGCGGCGGCTTCACTTGGGTGCAAGGGTGGTTCCGC 700

701 CCCGGCGTGGGTTCCTGAGGCTCAGGCCGTCCATTGCAGGAGCTGCTGGGCCGTCTGAAGGACGCAGTTT 770
                                                  GluLeuLeuGlyArgLeuLysAspAlaValS
```

FIG.5A

```
771   CAGAGCTGCAGGCAGAGCAGTTGGCCCTGGAACCCCTGCACCGGAGCCACAGCCCCGCAGAAGCCCCGGA   840
      erGluLeuGlnAlaGluGlnLeuAlaLeuGluProLeuHisArgSerHisSerProAlaGluAlaProGl

841   GGCCGGAGGAACGCCCCGTGGGGTCCTTGCACCCCATGACAGTGTCCTCCAGGCCCTGAGAAGACTACGC   910
      uAlaGlyGlyThrProArgGlyValLeuAlaProHisAspSerValLeuGlnAlaLeuArgArgLeuArg

911   AGCCCCAAGATGATGCACAAGTCAGGGTGCTTTGGCCGGAGGCTGGACCGGATCGGCTCCCTCAGTGGCC   980
      SerProLysMetMetHisLysSerGlyCysPheGlyArgArgLeuAspArgIleGlySerLeuSerGlyL

981   TGGGCTGCAATGGTAAGCCGCCTCCCTGCCGCCTTGGCTCCCCCTCCCCAGCCCCCTGGGTTCGACCCTT   1050
      euGlyCysAsnV

1051  GGAACCCCTTCTGGGTTTGTTGTCTCGGGGGATCACACTCTGAGGAAAGGACATCTGGACATCGCTCCTT   1120

1121  CTTGCTGACAGTCCTAAGGGCCAAGGAGTACGTTTCTGGAAATACTACGTGTGGACATCGTTGTCCAGGG   1190

1191  TCCCTACCCACCTCCTAGCCCCCTCCTGCCTCTCGCACCCAAAGGGCAGAATCATCTTAGGATGGAATCA   1260

1261  GTCGTTGTCTGGAAGCATCTCCTTGGAGCAGAAAGAGTCCTAAACATCGTCCTCGTAGCTCTCTCTGTCT   1330

1331  GTCTGTAGCCACGAAGGCAGAGGTCAGGGTCACCAGGGCAGTGATGATTCCCAGTTAACAGAGGAGGAGA   1400

1401  CTGAGGTCTAGAGAGATGGATTATTCCAAAGCCTCAAACATCCAGATCGGCTGAGGGTGGGGTTGGTGGC   1470

1471  AGGGATGGCTCCTGGGCTTGGGAAGCTCGGATCCTGCCTCAGTCTCCCACCTGACGCCATCATCCCCCTC   1540

1541  TCTCTCCTCCCACAGTGCTGAGAAAGTATTAAGGAGGAAGTCCCGACTGCCCACATCTGCATTGGATTCT   1610
```

FIG.5B

```
            alLeuArgLysTyr***
1611  TCAGCAGCCCCTGAGCCCCTTGGAAGCAGATCTTATTTATTCGTATTTATTTATTTATTTATTTCGATTG  1680
1681  TTTTATATAAGATGATCCTGACGCCCGAGCACGGATTTTCCACGGTGAAATAAAGTCAACCTTAGAGCTT  1750
1751  CTTTTGAAACCGATTTGTCCCTGTGCATTAAAAGTAACACATCATTTAAAAAAA  1804
```

FIG.5C

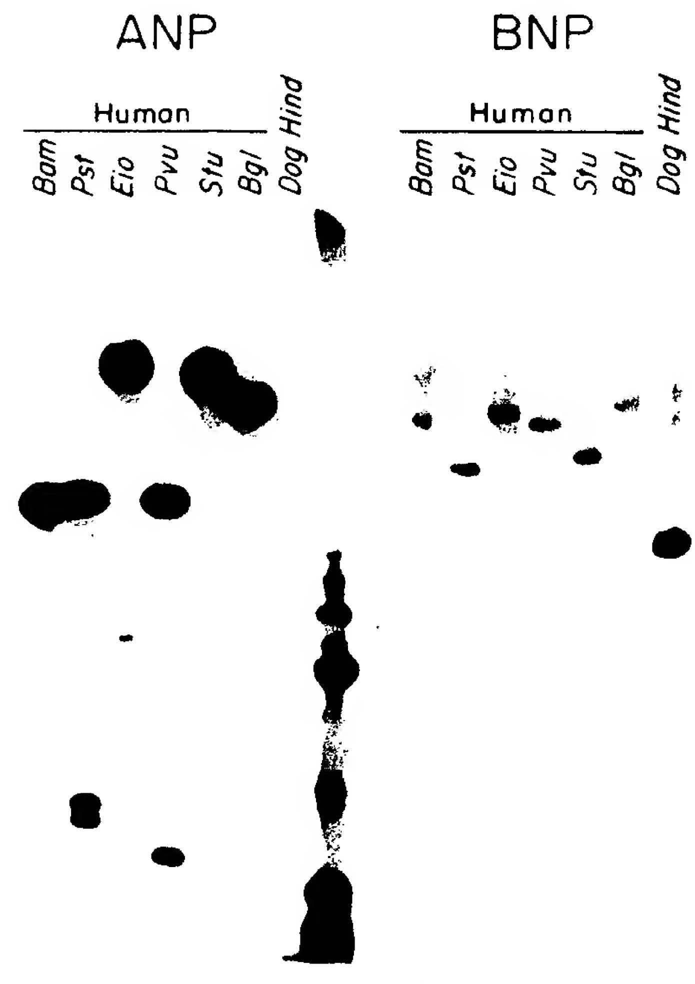
ANP
BNP
Human
Human
Bam
Pst
Eio
Pvu
Stu
Bgl
Dog Hind
Bam
Pst
Eio
Pvu
Stu
Bgl
Dog Hind

FIG.6

Human BNP Gene 12-12-88

```
  1  CCCACGGTGTCCCGAGGAGCCAGGAGGAGCACCCCGCAGGCTGAGGGCAGGTGGGAAGCAAACCCGGACG   70

 71  CATCGCAGCAGCAGCAGCAGCAGCAGAAGCAGCAGCAGCAGCCTCCGCAGTCCCTCCAGAGACATGGATC  140
                                                                   MetAspP

141  CCCAGACAGCACCTTCCCGGGCGCTCCTGCTCCTGCTCTTCTTGCATCTGGCTTTCCTGGGAGGTCGTTC  210
     roGlnThrAlaProSerArgAlaLeuLeuLeuLeuLeuPheLeuHisLeuAlaPheLeuGlyGlyArgSe

211  CCACCCGCTGGGCAGCCCCGGTTCAGCCTCGGACTTGGAAACGTCCGGGTTACAGGTGAGAGCGGAGGGC  280
     rHisProLeuGlySerProGlySerAlaSerAspLeuGluThrSerGlyLeuGln

281  AGCTCAGGGGGATTGGACAGCAGCAATGAAAGGGTCCTCACCTGCTGTCCCAAGAGGCCCTCATCTTTCC  350

351  TTTGGAATTAGTGATAAAGGAATCAGAAAATGGAGAGACTGGGTGCCCTGACCCTGTACCCAAGGCAGTC  420

421  GGTTCACTTGGGTGCCATGAAGGGCTGGTGAGCCAGGGGTGGGTCCCTGAGGCTTGGACGCCCCCATTCA  490

491  TTGCAGGAGCAGCGCAACCATTTGCAGGGCAAACTGTCGGAGCTGCAGGTGGAGCAGACATCCCTGGAGC  560
         GluGlnArgAsnHisLeuGlnGlyLysLeuSerGluLeuGlnValGluGlnThrSerLeuGluP

561  CCCTCCAGGAGAGCCCCCGTCCCACAGGTGTCTGGAAGTCCCGGGAGGTAGCCACCGAGGGCATCCGTGG  630
     roLeuGlnGluSerProArgProThrGlyValTrpLysSerArgGluValAlaThrGluGlyIleArgGl

631  GCACCGCAAAATGGTCCTCTACACCCTGCGGGCACCACGAAGCCCCAAGATGGTGCAAGGGTCTGGCTGC  700
     yHisArgLysMetValLeuTyrThrLeuArgAlaProArgSerProLysMetValGlnGlySerGlyCys
```

FIG.7A

```
701   TTTGGGAGGAAGATGGACCGGATCAGCTCCTCCAGTGGCCTGGGCTGCAAAGGTAAGCACCCCCTGCCAC   770
      PheGlyArgLysMetAspArgIleSerSerSerSerGlyLeuGlyCysLysV

771   CCCGGCCGCCTTCCCCCATTCCAGTGTGTGACACTGTTAGAGTCACTTTGGGGTTTGTTGTCTCTGGGAA   840

841   CCACACTCTTTGAGAAAAGGTCACCTGGACATCGCTTCCTCTTGTTAACAGCCTTCAGGGCCAAGGGGTG   910

911   CCTTTGTGGAATTAGTAAATGTGGGCTTATTTCATTACCATGCCCACAATACCTTCTCCCCACCTCCTAC   980

981   TTCTTATCAAAGGGGCAGAATCTCCTTTGGGGGTCTGTTTATCATTTGGCAGCCCCCCAGTGGTGCAGAA   1050

1051  AGAGAACCAAACATTTCCTCCTGGTTTCCTCTAAACTGTCTATAGTCTCAAAGGCAGAGAGCAGGATCAC   1120

1121  CAGAGCAATGATAATCCCCAATTTACAGATGAGGAAACTGAGGCTCAGAGAGTTGCATTAAGCCTCAAAC   1190

1191  GTCTGATGACTAACAGGGTGGTGGGTGGCACACGATGAGGTAAGCTCAGCCCCTGCCTCCATCTCCCACC   1260

1261  CTAACCATCATCACCCTCTCTCTTTCCCTGACAGTGCTGAGGCGGCATTAAGAGGAAGTCCTGGCTGCAG   1330
                                        alLeuArgArgHis***

1331  ACACCTGCTTCTGATTCCACAAGGGGCTTTTTCCTCAACCCTGTGGCCCTCATCTTTCCTTTGGAATTAG   1400

1401  TGATAAAGGAATCAGAAAATGGAGAGACTGGGTGCCCTGACCCTGTACCCAAGGCAGTCGGTTCACTTGG   1470

1471  GTGCCATGAAGGGCCTGGTGAGCCAGGGGTTGGGTCCCTGAGGCTTTTA   1519
```

FIG.7B

```
    Pig PreproBNF
    Dog PreproNRP
    Human PreproNRP
                                             10                                      20
1   Met Gly Pro Arg Met Ala Leu Pro Arg Val Leu Leu Leu     Leu Phe Leu His Leu Leu Leu
2   --- Glu --- Cys Ala --- --- --- --- Ala --- --- --- Leu --- --- --- --- --- Ser Pro
3   --- Asp --- Gln Thr --- Pro Ser --- Ala --- --- --- --- --- --- --- --- --- Ala Phe
                                             30                                  40

    Leu Gly Cys Arg Ser His Pro Leu Gly Gly Ala Gly Leu Ala Ser Glu Leu Pro Gly Ile
    --- --- Gly --- Pro --- --- --- --- --- Arg Ser Pro --- --- --- Ala Ser Glu Ala
    --- --- Gly --- --- --- --- --- --- Ser Pro --- Ser --- --- Asp --- Glu Thr Ser
                        ↑SP
        ↓1                                   50                                  60
    Gln Glu Leu Leu Asp Arg Leu Arg Asp Arg Val Ser Glu Leu Gln Ala Glu Arg Thr Asp
    Ser --- --- --- Gly --- --- Lys --- Ala --- --- --- --- --- --- --- Gln Leu Ala
    Gly --- Gln Arg Asn His --- Gln Gly Lys Leu --- --- --- --- Val --- Gln --- Ser
       ↑Leu Gln
                                             70                                  80
    Leu Glu Pro Leu Arg Gln Asp Arg Gly Leu Thr Glu Ala Trp Glu Ala Arg Glu Ala Ala
    --- --- --- --- --- His Arg Ser His Ser Pro Ala --- --- Pro --- --- Gly Gly Thr
    --- --- --- --- Gln Glu Ser Pro Arg Pro --- Gly Val --- Lys Ser --- --- Val ---

                                             90                                  100
    Pro Thr Gly Val Leu Gly Pro Arg Ser Ser Ile Phe Gln Val Leu Arg Gly Ile Arg Ser
    --- Arg --- --- --- Ala --- His Asp --- Val Leu --- Ala --- --- Arg Leu --- ---
    Thr Glu --- Ile Arg Gly His --- Lys Met Val Leu Tyr Thr --- --- Ala Pro --- ---
                                                                                 ↑1
                                             110                                 120
    Pro Lys Thr Met Arg Asp Ser Gly Cys Phe Gly Arg Arg Leu Asp Arg Ile Gly Ser Leu
    --- --- Met --- His Lys --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    --- --- Met Val Gln Gly --- --- --- --- --- --- Lys Met --- --- --- Ser --- Ser
            ↑?          ↑2
                                         130 131
    Ser Gly Leu Gly Cys Asn Val Leu Arg Arg Tyr
    --- --- --- --- --- --- --- --- --- Lys ---
    --- --- --- --- --- Lys --- --- --- --- His
```

FIG.8